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                GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - protein search, using frame_plus_n2p model

Run on:　February 1, 2005, 13:18:03 ; Search time 28.5 Seconds
　　　　　　　　　　　　　　　　(without alignments)
　　　　　　　　　　　　　　2694.605 Million cell updates/sec

Title:　　US-10-659-782A-11
Perfect score:　1030
Sequence:　1 actccggatgggtgctgtt........tggcagcgaggagggtgggg 579

Scoring table:　BLOSUM62
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　　　Ygapop 10.0 , Ygapext 0.5
　　　Fgapop 6.0 , Fgapext 7.0
　　　Delop 6.0 , Delext 7.0

Searched:　　478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters:　　956278

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:　Minimum Match 0%
　　　　　　　　　Maximum Match 100%
　　　　　　　　　Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :　Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match	Length	DB	ID	Description
	1	326	31.7	117	3	US-09-046-479-2	Sequence 2, Appli
	2	326	31.7	117	3	US-08-822-897C-2	Sequence 2, Appli
	3	326	31.7	117	4	US-09-608-810A-4	Sequence 4, Appli
	4	326	31.7	117	4	US-09-404-417A-2	Sequence 2, Appli
	5	326	31.7	117	4	US-10-140-002-442	Sequence 442, App
c	6	117	11.0	181	4	US-09-252-991A-26538	Sequence 26538, A
c	7	110.5	10.7	159	4	US-09-252-991A-30696	Sequence 30696, A
	8	110.5	10.7	550	4	US-09-616-289-47	Sequence 47, Appl
	9	109.5	10.6	355	3	US-08-483-533-41	Sequence 41, Appl
	10	109.5	10.6	355	4	US-09-283-471A-41	Sequence 41, Appl
	11	109.5	10.6	355	5	PCT-US91-06532-3	Sequence 3, Appl
c	12	108	10.1	174	4	US-09-252-991A-19399	Sequence 19399, A
	13	107.5	10.4	428	4	US-09-252-991A-24452	Sequence 24452, A
c	14	105	9.8	164	4	US-09-252-991A-20615	Sequence 20615, A
c	15	105	10.2	409	4	US-09-489-039A-17910	Sequence 17910, A
	16	105	9.8	491	4	US-09-489-039A-7836	Sequence 7836, Ap
	17	103.5	10.0	366	4	US-09-252-991A-17018	Sequence 17018, A
c	18	103.5	9.7	427	4	US-09-252-991A-17391	Sequence 17391, A
	19	103	9.7	164	4	US-09-252-991A-30154	Sequence 30154, A
c	20	103	9.7	201	4	US-09-252-991A-19786	Sequence 19786, A
c	21	103	9.7	355	3	US-08-483-533-41	Sequence 41, Appl
c	22	103	9.7	355	4	US-09-283-471A-41	Sequence 41, Appl
c	23	103	9.7	355	5	PCT-US91-06532-3	Sequence 3, Appl
	24	103	10.0	538	5	US-09-616-289-43	Sequence 43, Appl
c	25	102.5	9.6	206	4	US-09-252-991A-31481	Sequence 31481, A
	26	102.5	10.0	299	4	US-09-252-991A-22335	Sequence 22335, A
	27	102	9.9	505	4	US-09-252-991A-18964	Sequence 18964, A
c	28	101.5	9.5	249	4	US-09-252-991A-32877	Sequence 32877, A
c	29	101.5	9.5	348	4	US-09-252-991A-19087	Sequence 19087, A
	30	101.5	9.9	418	4	US-09-252-991A-32633	Sequence 32633, A
c	31	101.5	9.5	1142	4	US-09-252-991A-18234	Sequence 18234, A
c	32	101.5	9.5	1593	3	US-08-628-829-4	Sequence 4, Appli
c	33	101	9.5	215	4	US-09-252-991A-28157	Sequence 28157, A
c	34	100.5	9.4	162	4	US-09-252-991A-32485	Sequence 32485, A
c	35	100.5	9.4	1044	4	US-09-252-991A-18853	Sequence 18853, A
	36	99.5	9.7	152	4	US-09-252-991A-31484	Sequence 31484, A
	37	99	9.3	1150	4	US-09-252-991A-24671	Sequence 24671, A
c	38	98.5	9.2	217	4	US-09-252-991A-19862	Sequence 19862, A
c	39	98.5	9.2	257	4	US-09-252-991A-31869	Sequence 31869, A
	40	98.5	9.6	456	4	US-09-252-991A-19417	Sequence 19417, A
c	41	98.5	9.2	587	4	US-09-252-991A-22704	Sequence 22704, A
c	42	97.5	9.1	196	4	US-09-252-991A-23046	Sequence 23046, A
	43	97.5	9.1	335	4	US-09-252-991A-24899	Sequence 24899, A
c	44	97.5	9.1	575	4	US-09-252-991A-20649	Sequence 20649, A
c	45	97.5	9.1	684	4	US-09-252-991A-27004	Sequence 27004, A

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09044479
; Patent No. 6291653
; GENERAL INFORMATION:
;　APPLICANT: Sheppard, Paul O.
;　APPLICANT: Deisher, Theresa A.
;　TITLE OF INVENTION: MOTILIN HOMOLOGS
;　NUMBER OF SEQUENCES: 7
;　CORRESPONDENCE ADDRESS:
;　ADDRESSEE: ZymoGenetics, Inc.
;　STREET: 1201 Eastlake Avenue East
;　CITY: Seattle
;　STATE: WA
;　COUNTRY: USA
;　ZIP: 98102
;　COMPUTER READABLE FORM:
;　MEDIUM TYPE: Diskette
;　COMPUTER: IBM Compatible
;　OPERATING SYSTEM: DOS
;　SOFTWARE: FastSEQ for Windows Version 2.0
;　CURRENT APPLICATION DATA:
;　APPLICATION NUMBER: US/09/046,479
;　FILING DATE:
;　CLASSIFICATION:
;　PRIOR APPLICATION DATA:
;　APPLICATION NUMBER:
;　FILING DATE:
;　ATTORNEY/AGENT INFORMATION:
;　NAME: Sawislak, Deborah A
;　REGISTRATION NUMBER: 37,438
;　REFERENCE/DOCKET NUMBER: 97-04
;　TELECOMMUNICATION INFORMATION:
;　TELEPHONE: 206-442-6672
;　TELEFAX: 206-442-6678
;　TELEX:

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;       INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 117 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       FRAGMENT TYPE: internal
US-09-046-479-2

Alignment Scores:
Pred. No.:
Score:                      1.57e-25          Length:         117
                            326.00            Matches:        74
Percent Similarity:         53.19%            Conservative:   1
Best Local Similarity:      52.48%            Mismatches:     0
Query Match:                31.65%            Indels:         66
DB:                         3                 Gaps:           1

US-10-659-782A-11 (1-579) x US-09-046-479-2 (1-117)

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Db    1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20

Qy  172 GCCATGGCAGGCTTCCAGCTTCCTGAGCCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 231
            ||||||||||||||||||||||||||||||||||||  :::
Db   21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGln--Gln------- 37

Qy  232 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 291
Db   37 ------ 37

Qy  292 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 351
Db   37 ------ 37

Qy  352 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 411
Db   37 ------ 37

Qy  412 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTCTAGCAGGCT 471
            ||||||||||||||||||||||||||||||||||||||
Db   38 ------ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAlaLeuAlaGlyT 56

Qy  472 GGCTCCGCCCGGAAGATGAGGAGGTCAAGCAGCAGAGGGGCAGAGGATGAACTGGAAGTCCGG 530
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Db   56 rpLeuArgProGluAspGlyGlyGlyGlnAlaGluGlyAlaGluGlyLeuGluGluValArg 75

RESULT 2
US-08-822-897C-2
;    Sequence 2, Application US/08822897C
     Patent No. 6380158
GENERAL INFORMATION:
     APPLICANT: Sheppard, Paul O.
     APPLICANT: Deisher, Theresa A.
     TITLE OF INVENTION: MOTILIN HOMOLOGS
     NUMBER OF SEQUENCES: 7
     CORRESPONDENCE ADDRESS:
        ADDRESSEE: ZymoGenetics, Inc.
        STREET: 1201 Eastlake Avenue East
        CITY: Seattle
        STATE: WA
        COUNTRY: USA
        ZIP: 98102
     COMPUTER READABLE FORM:
        MEDIUM TYPE: Diskette
        COMPUTER: IBM Compatible
        OPERATING SYSTEM: DOS
        SOFTWARE: FastSEQ for Windows Version 2.0
     CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/822,897C
        FILING DATE:
        CLASSIFICATION: 536
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;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;       NAME: Sawislak, Deborah A
;       REGISTRATION NUMBER: 37,438
;       REFERENCE/DOCKET NUMBER: 97-04
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 206-442-6672
;       TELEFAX: 206-442-6678
;       TELEX:
;    INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 117 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       FRAGMENT TYPE: internal
US-08-822-897C-2

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Pred. No.:
Score:                      1.57e-25          Length:         117
                            326.00            Matches:        74
Percent Similarity:         53.19%            Conservative:   1
Best Local Similarity:      52.48%            Mismatches:     0
Query Match:                31.65%            Indels:         66
DB:                         3                 Gaps:           1

US-10-659-782A-11 (1-579) x US-08-822-897C-2 (1-117)

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Db    1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20

Qy  172 GCCATGGCAGGCTTCCAGCTTCCTGAGCCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 231
            ||||||||||||||||||||||||||||||||||||  :::
Db   21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGln--Gln------- 37

Qy  232 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 291
Db   37 ------ 37

Qy  292 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 351
Db   37 ------ 37

Qy  352 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 411
Db   37 ------ 37

Qy  412 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTCTAGCAGGCT 471
            ||||||||||||||||||||||||||||||||||||||
Db   38 ------ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAlaLeuAlaGlyT 56

Qy  472 GGCTCCGCCCGGAAGATGAGGAGGTCAAGCAGCAGAGGGGCAGAGGATGAACTGGAAGTCCGG 530
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Db   56 rpLeuArgProGluAspGlyGlyGlyGlnAlaGluGlyAlaGluGlyLeuGluGluValArg 75

RESULT 3
US-09-608-810A-4
;    Sequence 4, Application US/09608810A
     Patent No. 6420521
;    GENERAL INFORMATION:
     APPLICANT: Sheppard, Paul O.
     APPLICANT: Jaspers, Stephen R.
     APPLICANT: Deisher, Theresa A.
     APPLICANT: Bishop, Paul D.
     TITLE OF INVENTION: SGIP PEPTIDES
     FILE REFERENCE: 99-51
     CURRENT APPLICATION NUMBER: US/09/608,810A
     CURRENT FILING DATE: 2000-06-30
     PRIOR APPLICATION NUMBER: 60/141,592
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; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4

Alignment Scores:
Pred. No.:            1.57e-25        Length:        117
Score:               326.00          Matches:       74
Percent Similarity:  53.19%          Conservative:  1
Best Local Similarity: 52.48%        Mismatches:    0
Query Match:         31.65%          Indels:        66
DB:                  4               Gaps:          1

US-10-659-782A-11 (1-579) x US-09-608-810A-4 (1-117)

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Qy  172 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 231
            |||||||||||||||||||||||||||||||||||||||||   ::
Db   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln------Gln 37

Qy  232 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 291
Db   37 ------ 37

Qy  292 CAGCAGCGCGCCATCTCTGGGCTTCAGTCTTCTTCCCCAGAGCACAAAGGACTCTGGGTCTGAC 351
Db   37 ------ 37

Qy  352 CTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 411
Db   37 ------ 37

Qy  412 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCCCGAGCTCAGCAGGCT 471
            |||||||||||||||||||||||||||||||||||||||||||||||
Db   38 -----ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAlaLeuAlaLeuGlyT 56

Qy  472 GGCTCCGCCCGGAAGATGAGGTCAAGCAGAAGGGGCAGAGGATGAACTGGAAGTCCGG 530
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Db   56 rpLeuArgProGluAspGlyGlnAlaGluGlyAlaGluGluAspGluLeuGluValArg 75
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RESULT 4
US-09-404-417A-2
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; Sequence 2, Application US/09404417A
; Patent No. 6627729
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: TML PEPTIDES
; FILE REFERENCE: 97-04C1
; CURRENT APPLICATION NUMBER: US/09/404,417A
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-417A-2

Alignment Scores:
Pred. No.:  1.57e-25     Length:   117
Score:      326.00       Matches:  74
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Percent Similarity:     53.19%        Conservative:  1
Best Local Similarity:  52.48%        Mismatches:    0
Query Match:            31.65%        Indels:        66
DB:                     4             Gaps:          1

US-10-659-782A-11 (1-579) x US-09-404-417A-2 (1-117)

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Db    1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20

Qy  172 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 231
Db   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln------Gln 37

Qy  232 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 291
Db   37 ------ 37

Qy  292 CAGCAGCGCGCCATCTCTGGGCTTCAGTCTTCTTCCCCAGAGCACAAAGGACTCTGGGTCTGAC 351
Db   37 ------ 37

Qy  352 CTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 411
Db   37 ------ 37

Qy  412 AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCCCGAGCTCAGCAGGCT 471
Db   38 -----ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAlaLeuAlaLeuGlyT 56

Qy  472 GGCTCCGCCCGGAAGATGAGGTCAAGCAGAAGGGGCAGAGGATGAACTGGAAGTCCGG 530
Db   56 rpLeuArgProGluAspGlyGlnAlaGluGlyAlaGluGluAspGluLeuGluValArg 75
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RESULT 5
US-10-140-002-442
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; Sequence 442, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT:  Baker,Kevin P.
; APPLICANT:  Beresini,Maureen
; APPLICANT:  DeForge,Laura
; APPLICANT:  Desnoyers,Luc
; APPLICANT:  Filvaroff,Ellen
; APPLICANT:  Gao,Wei-Qiang
; APPLICANT:  Gerritsen,Mary E.
; APPLICANT:  Goddard,Audrey
; APPLICANT:  Godowski,Paul J.
; APPLICANT:  Gurney,Austin L.
; APPLICANT:  Sherwood,Steven
; APPLICANT:  Smith,Victoria
; APPLICANT:  Stewart,Timothy A.
; APPLICANT:  Tumas,Daniel
; APPLICANT:  Watanabe,Colin K
; APPLICANT:  Wood,William
; APPLICANT:  Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 442
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-002-442

Alignment Scores:
Pred. No.:  1.57e-25     Length:   117
Score:      326.00       Matches:  74
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Percent Similarity:     53.19%        Conservative:    1
Best Local Similarity:  52.48%        Mismatches:      0
Query Match:            31.65%        Indels:          66
DB:                     4             Gaps:            1

US-10-659-782A-11 (1-579) x US-10-140-002-442 (1-117)

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Db    1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20

Qy  172 GCCATGGCAGGCTCCAGCTTCCTGAGCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 231
        |||||||||||||||||||||||||||||||||| :::
Db   21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln------ 37

Qy  232 CACAAAGCCCCACATGTTGTCCGACTTAGCAACCAGCTCTGTGACCTGGAG 291
Db   37 --------------------------------------------------- 37

Qy  292 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAAGGACTCTGGGTCTGAC 351
Db   37 --------------------------------------------------- 37

Qy  352 CTCACTGTTTCTGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCC 411
Db   37 --------------------------------------------------- 37

Qy  412 AGCAGAAAGAGTCGAAGAAGCCACCAGCCAAGCTGCAGCCCGAGCTCTAGCAGGCT 471
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   38 ----ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAlaLeuAlaGlyT 56

Qy  472 GGCTCCGCCCGGAAGATGGAGGTCAACGCAGAAGGGGCAGAGGATGAACTGGAAGTCCGG 530
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   56 rpLeuArgProGluArgProGluGlnGlnAlaGlyGlnAlaGluGluAspGluLeuGluValArg 75
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RESULT 6
US-09-252-991A-26538
; Sequence 26538, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26538
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26538

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Alignment Scores:
Pred. No.:               0.000927        Length:         181
Score:                   117.00          Matches:        43
Percent Similarity:      34.62%          Conservative:   11
Best Local Similarity:   27.56%          Mismatches:     30
Query Match:             10.97%          Indels:         72
DB:                      4               Gaps:           8

US-10-659-782A-11 (1-579) x US-09-252-991A-26538 (1-181)

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Qy  289 CCAGGTCACAGAGCTGGTTGCTAAGTGGCAGGGCTGGAACACATGTGGGGCTTTGTGGG 230
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Db   64 ProGlySerArgAlaGlySer--------- 70

Qy  229 GAGGTCTCACTGGACTTCTGTCTGTTCAGGCTCAGGA------- AGC 188
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Db   71 -----AlaProAlaGlySerGlyCysArgGlyCysArgGlySerGlyArgSerProHisArgArgAlaAla 88

Qy  187 TGG--------- AGCCTGCCATGGCCAAGTCCA 164
        |||  :::
Db   89 TrpLeuArgGlyProAlaSerValHisAspHisGlySerAlaAlaProGlyProAlaPro 108

Qy  163 GCCAGAGCATCCGAGAGGAGCAGGAGGCTGCAGACGGTCCCTGGGAGG--------- 116
        |||||||||||||||||||
Db  109 AlaArgArgPheProAlaThrGlyGlyCysArgArgGlyGlyArgProGlyGlyGlyCys 128

Qy  115 ---------GCATGG 110
        ^
Db  129 ProLeuHisArgTyrProAlaArgTrpAlaThrAlaGluProAlaTrpProArgProLeu 148

Qy  109 ---CCTCAGCTGGGTTGCAGACAGGTGGGCCTGCCGTCTGCGGAGGTGGTGCCTGTGCT 53
        ||| ::: :::||||
Db  149 ProProAlaArgGlyTyrTrpArgThrArgHisArgArgProTrpProThrGly------ 165

Qy   52 GTCAGGTCTTATATAGGAGACGGCGTTTGTCTAAACAGCACCCATCCA 5
        ::: |||||
Db  166 -----------------------------ValArgSerAlaHisPro 171
```

RESULT 7
US-09-252-991A-30696
; Sequence 30696, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30696
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30696

```
Alignment Scores:
Pred. No.:               0.00417         Length:         159
Score:                   110.50          Matches:        53
Percent Similarity:      39.31%          Conservative:   15
Best Local Similarity:   30.64%          Mismatches:     51
Query Match:             10.36%          Indels:         54
DB:                      4               Gaps:           11

US-10-659-782A-11 (1-579) x US-09-252-991A-30696 (1-159)

Qy  520 AGTTCATCCTCCTGCCCCTTCGTGCTTGACCTCCATCTTCCGGCGGAGCCAGCCTGCTAGA 461
        ::::||||| ::: |||| :::||||||
Db    7 AlaThrSerArgSerProArgAlaArgProProSerThr----ArgCysSerProAla-Se 25

Qy  460 GCTCGGGGCTGCAGCTTGGCTGGTGGCTTCTTCG--------- ACTCCTTT 419
        ::: |||||||
Db   25 rValSerSerAlaAlaAspArgThrSerSerGlyGlnSerProSerThrCysSerProCy 45

Qy  418 CTCTGCTGAAGGGGAAAACAGTCTGTTAGGACTTAAGCCCCATGTCCTTCCAGAAA 359
        ::::: :::
Db   45 sSerSerAla------------------AlaProProCys 53

Qy  358 CAGTGAGGTCAGACCCAGAGTCCTTTGTGCTCTGGGAGAAGAGCCCAGAGATGGC 299
        |||||||
Db   54 -SerArgCysSerProArgThrSerCysSerProGlyProGlyAlaSer---------Al 70
```

```
Qy   298 GCTGCTGCTCCAGGTCACAGAGCTGGTTGCTAAGTGGCAGGGCTGGAACAACATGTGGGG 239
             |||||||||:::|||||    |||                              :  |||
Db    70 a-CysCysAlaArgLeuGlnArgTrp----------AlaProTrpArgCysArgS  85

Qy   238 CTTTGTGGGGAGGTCTCACCTGGACTCTCGGTTGTTCAGGGCTCAGGAAGCTGGAGCCTG 179
            ::   |||  ||                                |||||  ||
Db    85 erGlyTyr-ArgThrSer-----AlaSerAsnAlaThrSerGlyGlySerCysSerSer 102

Qy   178 CCAGTG-------CCAAGTCCAGCCAGAGAGCATGCCGAGGAGCAGGAGGC 137
            |||||||||:::::||||||||||||
Db   103 ProTrpAlaSerSerAlaTrpProSerProSer---AlaCysArgAsnArgSerGly 121

Qy   136 TGCAGACGG------------TCCCTGGGGAGGGCATGGCCTCAGCTGGGGTTGCAGA 92
            |||                              |||
Db   122 CysProSerAlaCysTrpTrpTyrSerAlaProArgThrTrp----- 135

Qy    91 CAGGTGGGCCTGCAGTCCTGGCGGAGTGGTGCC 59
            :::|||  |||   |||
Db   136 -----------SerAlaTrpSerAlaAla 142
```

```
Alignment Scores:
Pred. No.:              0.00677       Length:           550
Score:                  110.50        Matches:           56
Percent Similarity:     37.38%        Conservative:      24
Best Local Similarity:  26.17%        Mismatches:        59
Query Match:            10.73%        Indels:            75
DB:                     4             Gaps:              10

US-10-659-782A-11 (1-579) x US-09-616-289-47 (1-550)
```

```
Qy    29 GCCGTCTCCTAT-----------ATAAGACCTGACAGCACAGGACCACTCCGCCA 73
            :::::|||||||          :::::|||
Db    91 SerIleSerTyrArgArgAsnAlaAlaArgValGlnProProArgArgGlyAlaThrProPro 110

Qy    74 -------------GGACTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCA 112
                                 :::|||
Db   111 AlaProProArgAlaProArgArgGlyGlyProAlaAlaAlaAlaAlaAlaProProThrPro 130

Qy   113 TGCCCTCCCCAGGGACACCGTCTGCAGCCTCCTGCTCCTCCGGCATGCTCTGGCTGGACTTGG 172
            |||||                 :::  ||    ||||||
Db   131 AlaProAlaProProProAlaProValAlaAlaAlaAlaAla------- 144
```

```
Qy   173 CCATGCAGGTCCA 217
            :::||||||
Db   145 ProAlaArgAlaProArgAlaAlaAlaAlaAlaAlaAlaAlaThr-AlaProProSerPr 164

Qy   218 AGGTGAGACCTCCCA--------------CAAAGCCCACATGTGTTCCAGCCC 259
            |||                              :::|||
Db   164 oGlyProAlaGlnProGlyProArgAlaProArgAlaAlaProLeuAlaAlaProProPr 184

Qy   260 TGCCACTTAGCAACCAGCTCTGTGACCTGGACGAGCAGCAGCCGCCATCTCTGGGC------- 311
            |||||||||||:::|||||||||
Db   184 oAla-------ProAlaAla--ProProAlaAlaAlaProProAlaGlyProAlaProArgAr 200

Qy   312 ----------------------------------TTCAGTCTTCTCCCAGAGCACACAAAGG 337
                                               ||||||
Db   200 gAlaProProProAlaAlaAlaValAlaAlaAlaArgGluSerProLeuPro----- 216

Qy   338 ACTCTGGGTCTGACCTCACTGTTCTGGAGGACATGGGGCTTAGAGTCCTAAACACAGAC 397
            |||                              |||
Db   217 -----------------------------------ProProProGlnPr 221

Qy   398 TGTTTCCCCCTTCCAGCACAGAAAAGAGTCGAAGAAGCACCAGCCAAGCTGCAGCCCCG 457
            :::|||                              ||||||
Db   221 oProAlaProProGlnGlnGlnGlnProProProProProGlnGlnProGl 241

Qy   458 A----------------------------------GCTTCTAGCAGCTGGTGCTCCGCCCGGAAGATGGAGGTCA 496
            :                              :::  :::::
Db   241 nProProProGluProGlyGlyAlaGlyAlaGlyGly-GlyProAlaArgProValSerLeuA 261

Qy   497 AGCAGAAGGGGCAGAGGATGAACTGGAAGTCCGGGTCG 534
            ::::  :::  :::   |||||||
Db   261 rgGluValValArgTyrLeuGlyGlySerSerGlyAla 273
```

; APPLICANT: Chou, Joany
; TITLE OF INVENTION: Method For Treating Tumorigenic Diseases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/283,471A
; FILING DATE: 04-APR-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/861,233
; FILING DATE: 31-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/419,853
; FILING DATE: 11-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/483,533
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, James P.
; REGISTRATION NUMBER: 28,491
; REFERENCE/DOCKET NUMBER: 27373/32742A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-283-471A-41

Alignment Scores:
Pred. No.:   Length: 355
Score: 0.00725   Matches: 66
Percent Similarity: 33.75%   Conservative: 15
Best Local Similarity: 27.50%   Mismatches: 73
Query Match: 10.63%   Indels: 86
DB: Gaps: 13

US-10-659-782A-11 (1-579) x US-09-283-471A-41 (1-355)

```
Qy   44  AGACCTGACAGCACAGGCACCACTCCGCCAGGACTGCAGGCCCAC------------  88
         ||||||     ::            |||||||||||||||||||||||
Db   95  ArgProThrAlaAlaAlaAlaProArgProProGly------ProHisArgProAlaTrpAlaAla  112

Qy   89  CTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCCAGGACCGTCTGCA------------  136
         ||||              |||    ||||||||||||||:::
Db  113  ArgGlyAlaGlyLeuThrProProThrProProArgAlaProSerAlaPheArgArgAla  132

Qy  137  ------GCCTCCTGCTCCTCG----------------GCATGCTCTGGCTGG  166
         :::::|||::|||:|||                    |||||
Db  133  SerProSerAlaCysAlaSerProArgSerThrTrpArgAlaCysAsp-AlaAr  152

Qy  167  ACTTGGCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGAC  226
         ||||||       ||||||                ||||
Db  152  gAlaGlyArgGlyArgSerProProArgProProArgProProArgPro---ProAr  171

Qy  227  CTCCCCACAAAGCCCCACATGTTGTTCCAGCCCTGCCACT----------------  266
         ||||||    |||                    |||:::|||
Db  171  gProProArgProArgGlyCysAlaSerArgProThrSerGlyCysAlaThrTrpTr  191

Qy  267  ----------TAGCAACCAGCTCTGTGACCTGGAGCAGCAGCGCCATCTCTGGGCTTCAG  316
                   ||||       |||:::|||
Db  191  pSerGlyProAlaTrpProAlaTrpArgAlaAlaArgGlyProAlaSerGly------  209

Qy  317  TCTTCTCCCAGAGCACAAAGGACTCTGGGTCT--------GACCTCACTGTTTCTG  364
         |||||      ||::|||
Db  210  ------ProThrGlyLeuGly-SerGlyAlaGlyTrpArgArgProArgArgSerG  227

Qy  365  GAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCCAGGAGAGAAAGGA  424
         |||||     ||||||       ::     |||:||
Db  227  lyArgAlaTrpGlyProArgProValProGlyProTrpProProAlaGluProAlaArgArgT  247

Qy  425  GTCGAAGAAGCCACCACGCCAAGCTGCA--------------GCCCCCGAGCTCTAGC  466
         ::|||       |||                          |||||
Db  247  hrArgSerAsnValThrProGlu-AlaAlaTrpProAlaTrpPheArgArgGlyValAlaPheArgValPheArgArgGlyProArgGlyGlySerSer  266

Qy  467  ----------AGGCTGGCTCCGCCCGAAGAATGGAGGTCAAGCAGA--------------  502
         |||||       :::
Db  267  AlaProSerArgSerProGluArgArgTrpGlnGluProArgIleTyrThrLeuGlyAla  286

Qy  503  --------------------AGGGGCAGGAGGATGAAACTGGAAGTCCGGGTCGG  535
                             |||
Db  287  SerProProSerGlnGlyGlyProProArgGlyArgAsp------  299

Qy  536  TACCCTCTGCAGTTTTATGCTTCTGTCG----------CAGCGAGGAGGG  574
         |||||||||||              |:::
Db  300  ---------------------TrpProIleGlyLyArgGlnArgGlyGlyGly  309
```

RESULT 10
US-09-283-471A-41
; Sequence 41, Application US/09283471A
; Patent No. 6340673
; GENERAL INFORMATION:
; APPLICANT: Roizman, Bernard

; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-483-533-41

Alignment Scores:
Pred. No.:   Length: 355
Score: 0.00725   Matches: 66
Percent Similarity: 33.75%   Conservative: 15
Best Local Similarity: 27.50%   Mismatches: 73
Query Match: 10.63%   Indels: 86
DB: Gaps: 13

US-10-659-782A-11 (1-579) x US-08-483-533-41 (1-355)

```
Qy   44  AGACCTGACAGCACAGGCACCACTCCGCCAGGACTGCAGGCCCAC------------  88
         ||||||     ::            |||||||||||||||||||
Db   95  ArgProThrAlaAlaAlaAlaProArgProProGly------ProHisArgProAlaTrpAla  112

Qy   89  CTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCCAGGACCGTCTGCA------------  136
         ||||              |||    ||||||||||||||:::
Db  113  ArgGlyAlaGlyLeuThrProProThrProProArgAlaProSerAlaPheArgArgAla  132

Qy  137  ------GCCTCCTGCTCCTCG----------------GCATGCTCTGGCTGG  166
         :::::|||::|||:|||                    |||||
Db  133  SerProSerAlaCysAlaSerProArgSerThrTrpArgAlaCysAsp-AlaAr  152

Qy  167  ACTTGGCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGAC  226
         ||||||       ||||||                ||||
Db  152  gAlaGlyArgGlyArgSerProProArgProProArgProProArgPro--ProAr  171

Qy  227  CTCCCCACAAAGCCCCACATGTTGTTCCAGCCCTGCCACT----------------  266
         ||||||    |||                    |||:::|||
Db  171  gProProArgProArgGlyCysAlaSerArgProThrSerGlyCysAlaThrTrpTr  191

Qy  267  ----------TAGCAACCAGCTCTGTGACCTGGAGCAGCAGCGCCATCTCTGGGCTTCAG  316
                   ||||       |||:::|||
Db  191  pSerGlyProAlaTrpProAlaTrpArgAlaAlaArgGlyProAlaSerGly------  209

Qy  317  TCTTCTCCCAGAGCACAAAGGACTCTGGGTCT--------GACCTCACTGTTTCTG  364
         |||||      ||::|||
Db  210  ------ProThrGlyLeuGly-SerGlyAlaGlyTrpArgArgProArgArgSerG  227

Qy  365  GAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCCAGGAGAGAAAGGA  424
         |||||     ||||||       ::     |||:||
Db  227  lyArgAlaTrpGlyProArgProValProGlyProTrpProProAlaGluProAlaArgArgT  247

Qy  425  GTCGAAGAAGCCACCACGCCAAGCTGCA--------------GCCCCCGAGCTCTAGC  466
         ::|||       |||                          |||||
Db  247  hrArgSerAsnValThrProGlu-AlaAlaTrpProAlaTrpPheArgArgGlyValAlaPheArgValPheArgArgGlyProArgGlySerSer  266
```

Score: 109.50   Matches: 66
Percent Similarity: 33.75%   Conservative: 15
Best Local Similarity: 27.50%   Mismatches: 73
Query Match: 10.63%   Indels: 86
DB: 5   Gaps: 13

US-10-659-782A-11 (1-579) x PCT-US91-06532-3 (1-355)

```
Qy   44 AGACCTGACAGCACAGCCACCACTCCGCCAGGACTCGAGGCCCAC--------------   88
           |||||                 :::
Db   95 ArgProThrAlaAlaAlaProArgProProGly-------ProHisArgProAlaTrpAla  112

Qy   89 CGTGTCGCAACCCAGCTGAGGCCATGCCCTCCCCAGGAGACCGTCTGCA-----------  136
                                         ||||||| :::
Db  113 ArgGlyAlaGlyLeuThrProProThrProProAlaProSerAlaPheArgArgAla     132

Qy  137 ------GCCTCCTGCTCCTG-------------------GCAATGTCTGGCTGG         166
           :::::|||::||||::|||
Db  133 SerProSerAlaCysAlaSerProArgSerThrTrpArgAlaCysAlaCysAsp-AlaAr   152

Qy  167 ACTTGGCCATGGCAGCTCCAGCTTCCTGAGCCCTGAACACCAGAGGTCCAGTGAGAC     226
           ||||| ||||||       |||| |||
Db  152 gAlaGlyArgGlyArgGlyArgSerProArgProProProArgPro---ProAr      171

Qy  227 CTCCCCACAAAGCCCCACATGTTGTCCAGCCCTGCCACT-----------------     266
           ||::: |||     :::||
Db  171 gProProArgProProArgGlyCysAlaSerArgProThrSerGlyCysAlaThrTrpTr  191

Qy  267 --------TAGCAACCAGCTCGTGACCTGGACAGCAGCAGCGCCATCTCTGGGCTTCAG-----  316
                   ||||||
Db  191 pSerGlyProArgProProAlaTrpArgAlaAlaAlaArgGlyProAlaSerGly--------  209

Qy  317 TCTTCTCCCAGAGCACAAAGGACTCTGGGTCT----------------GACCTCACTGTTTCTG  364
           |||  :||||:
Db  210 ------ProThrGlyLeuGly-SerGlyAlaGlyThrArgArgProArgSerSerG          227

Qy  365 GAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCCAGCAGAGAAAAGGA    424
           ||||||||||        ::: :::|||
Db  227 lyArgAlaTrpGlyProArgProValProGlyProTrpProAlaGluProAlaGluArgArgt  247

Qy  425 GTCGAAGAAGCCACCAGCCAAGCTGCA----------------GCCCCGAGCTCTAGC        466
           ::||| |||        ::||
Db  247 hrArgSerAsnValThrProGlu-AlaAlaTrpValPheArgGlyAlaProGlySerSer    266

Qy  467 ------AGGCTGGCTCCGCCCCGGAAGATGGAGGTCAAGCAGA--------------     502
                 |||:::
Db  267 AlaProSerArgSerProGluArgArgTrpGlnGluProArgIleTyrThrLeuGlyAla    286

Qy  503 ---------------AGGGGCAGGAGGATGAACTGGAAGTCCGGGTCGG           535
                          ||||||||
Db  287 SerProProSerGlnGlyGlyProProArgGlyArgAsp-------------        299

Qy  536 TACCCTCTGCAGTTTTATGCTTCTGTGG---------CAGCGAGGAGGG     574
           |||||||||||||||
Db  300 -------------------------------TrpProIleGlyArgGlnArgGlyGlyGly  309
```

RESULT 11
PCT-US91-06532-3
; Sequence 3, Application PC/TUS9106532
; GENERAL INFORMATION:
;   APPLICANT: Roizman, Bernard
;   TITLE OF INVENTION: Recombinant Herpes Simplex Viruses
;   TITLE OF INVENTION: Vaccines and Methods
;   NUMBER OF SEQUENCES: 8
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
;   ADDRESSEE: Bicknell
;   STREET: Two First National Plaza Suite 2100
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: USA
;   ZIP: 60603
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US91/06532
;   FILING DATE: 19910910
;   CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Gruber, Lewis S.
;   REGISTRATION NUMBER: 30,060
;   REFERENCE/DOCKET NUMBER: 27373/8235
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 312/346-5750
;   TELEFAX: 312/984-9740
;   TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 355 amino acids
;   TYPE: AMINO ACID
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US91-06532-3

```
Db  171 gProProArgProProArgGlyCysAlaSerArgProThrSerGlyCysAlaThrTrpTr  191

Qy  267 --------TAGCAACCAGCTCGTGACCTGGACAGCAGCAGCGCCATCTCTGGGCTTCAG-----  316

Db  191 pSerGlyProArgProProAlaTrpArgAlaAlaAlaArgGlyProAlaSerGly--------  209

Qy  317 TCTTCTCCCAGAGCACAAAGGACTCTGGGTCT----------------GACCTCACTGTTTCTG  364

Db  210 ------ProThrGlyLeuGly-SerGlyAlaGlyThrArgArgProArgSerSerG          227

Qy  365 GAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCTTCCAGCAGAGAAAAGGA    424

Db  227 lyArgAlaTrpGlyProArgProValProGlyProTrpProAlaGluProAlaGluArgArgt  247

Qy  425 GTCGAAGAAGCCACCAGCCAAGCTGCA----------------GCCCCGAGCTCTAGC        466

Db  247 hrArgSerAsnValThrProGlu-AlaAlaTrpValPheArgGlyAlaProGlySerSer    266

Qy  467 ------AGGCTGGCTCCGCCCCGGAAGATGGAGGTCAAGCAGA--------------     502

Db  267 AlaProSerArgSerProGluArgArgTrpGlnGluProArgIleTyrThrLeuGlyAla    286

Qy  503 ---------------AGGGGCAGGAGGATGAACTGGAAGTCCGGGTCGG           535

Db  287 SerProProSerGlnGlyGlyProProArgGlyArgAsp-------------        299

Qy  536 TACCCTCTGCAGTTTTATGCTTCTGTGG---------CAGCGAGGAGGG     574

Db  300 -------------------------------TrpProIleGlyArgGlnArgGlyGlyGly  309
```

Alignment Scores:
Pred. No.:   0.00725   Length: 355

RESULT 12
US-09-252-991A-19399
; Sequence 19399, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;   APPLICANT: Marc J. Rubenfield et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;   TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE-REFERENCE: 107196.136
;   CURRENT APPLICATION NUMBER: US/09/252,991A
;   CURRENT FILING DATE: 1999-02-18
;   PRIOR APPLICATION NUMBER: US 60/074,788
;   PRIOR FILING DATE: 1998-02-18
;   PRIOR APPLICATION NUMBER: US 60/094,190
;   PRIOR FILING DATE: 1998-07-27
;   NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19399

```
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19399

Alignment Scores:
Pred. No.:              0.00785
Score:                  108.00
Percent Similarity:     34.86%          Length:        174
Best Local Similarity:  27.43%          Matches:       48
Query Match:            10.12%          Conservative:  13
                                        Mismatches:    66
                                        Indels:        48
                                        Gaps:          9

US-10-659-782A-11 (1-579) x US-09-252-991A-19399 (1-174)

Qy  577 CCACCCTCCTCGCTGCCACAGAAGCATAAAACTGCAGAGGTACCGACCCGGACTTCCAGT 518
            ||||||||||          :::::         |||  ||||||||
Db   11 ProProSer---------ArgArgSerGlyProAlaProVal-Pro---ArgAlaProGly 26

Qy  517 TCATCCTTCTGCCCCTTCTGCTTGACCTCCATCTCGGGCGGGAGCCAGCCTGCTAGAGCT 458
            |||||  :::|| ||          |||||||||
Db   27 SerAlaGlySerProArgAla--SerProGlyGlyCysArgIleProProArgArgArg 45

Qy  457 CGGGGCCTGCAGCTTGGCTGGCTTGGCTTCTTCGACTCCTTTCTCTGCTGGAGGGGGAAACA 398
            |||||||
Db   46 ArgGlySer------------SerPro 51

Qy  397 GTCTGTTTAGGACTCTAAGCCCCCATGTCCTTCCAGAAACAGTGAGGTCAGACCCCAGAGT 338
            |||       |||   :::      :::
Db   52 ValArgProGlyArgProGlyHisLeuArgArgAlaArgArgAlaAlaProArgPro 71

Qy  337 CCTTTGTCGTCTTGGGAGAAGACTGAAGCCCAGAGATGGCCGCTGCTTCCAGGTCACAGA 278
            ||||||  :::|  |||||||||||
Db   72 SerArgCysSerGlySerGlySerArgProArgSerGlyArgSerAlaProGlySerArg 91

Qy  277 GCTCGGTTGCTAAGTGAGCAGGCTGGAACAACATGTGGGGCTTTGTGGG---GAGGTCTCA 221
                               |||                    |||
Db   92 --------------------ArgThrProArgCysSerAlaProProSer 101

Qy  220 CCTGGGACTTCTCTGGTTCAGGGCTCAGGAAGCTGG-----AGCCTGCCATGCCCAAGT 167
               |||                               ||:
Db  102 Pro--------------------------------GlyArgArgTrpArgSerThrHrThrProGlyProGly 115

Qy  166 CCAGCCAGAGCCATGCCGAGGAGGAGGAGGGCTGCAGACGGTCCCTG-----122
            ||||||||||||     ::|||||||||
Db  116 SerArgArgLeuThrAlaGlyArgProGlyCysArgArgAspTrpProValArgThrGly 135

Qy  121 ------------------GGGAGGGCATGCCCTCAGCTCGGGTTGCAGA 92
                               ||:::   ::|||||||||
Db  136 LysArgArgArgProGlyArgSerHisProProValGlyCysArg 150
```

RESULT 13
US-09-252-991A-24452
; Sequence 24452, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;   APPLICANT: Marc J. Rubenfield et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;   TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 107196.136
;   CURRENT APPLICATION NUMBER: US/09/252,991A
;   CURRENT FILING DATE: 1999-02-18
;   PRIOR APPLICATION NUMBER: US 60/074,788
;   PRIOR FILING DATE: 1998-02-18
;   PRIOR APPLICATION NUMBER: US 60/094,190
;   PRIOR FILING DATE: 1998-07-27
;   NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24452
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24452

```
Alignment Scores:
Pred. No.:              0.0126
Score:                  107.50
Percent Similarity:     36.42%          Length:        428
Best Local Similarity:  28.32%          Matches:       49
Query Match:            10.44%          Conservative:  14
DB:                                     Mismatches:    70
                                        Indels:        40
                                        Gaps:          8

US-10-659-782A-11 (1-579) x US-09-252-991A-24452 (1-428)

Qy   44 AGACCTGACAGCAGGCACCACTCCGCCAGGACTGCAGGCCCACCTGTCTGCAACCCAG 103
             ||||||                                 :::||
Db  175 ArgAlaAspArgProGlyThrTyrAlaProGly--------ArgProGlnArg 189

Qy  104 CTGAGGCCATGCCCTCCCCAGGAGACCGTCTCGCAGCCTCCTCGGCATGCTCCTCGGC 163
             |||       |||
Db  190 LeuArgProLeuProSerAlaGlyProSerArgArg 201

Qy  164 TGGACTTGGCCATGCAGCGTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGA 223
             |||||  ||
Db  202 TrpArgLeu-HisGlyArgLeuLeuLeuProGlnCysArgHisProGlyVa 221

Qy  224 GACCTCCCCA---------------------CAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTA 268
             |||
Db  221 lProArgProGlyCysProAlaArgGlyAspProArgCysArgLeuSerProTrpGlnAr 241

Qy  269 GCAACCAGCTCTGTGACCTGGAGCAGCAGCCGCCATCTCGGGCTTCAGTCTTCTCCCAGA 328
             |||
Db  241 gHisPro--------------------GlyTyrLeuProProAr 250

Qy  329 GCACAAAGGACTCCTGGGTCTGACCTCACTGTTTCTCGGAAGGACATGGGGCTTAGAGTCC 388
             :::    :::                      :::
Db  250 gArgCysAlaValArgLeuAspPro--------------TrpArgSerAlaGly 263

Qy  389 TAAACAGACTGTTTCCCCCTTCCAGCAGAAGGAGTCGAAGAAGAAGAAGCCAAGCT 448
             :::||||  ::|||||||     :::||||
Db  264 -ArgIleProValLeuProArgLeuProArgArgArgArgArgArgArgArgGlyLe 283

Qy  449 GCAGCCCGAGCTCTAGCAGGC-----TGGCTCCGC--------CCCGGAAGATGGAGGTCAAGC 499
             |||||||:::                ||||||
Db  283 uGlnProGlnLeuSerAlaGlyProThrProTrpGlnArgLeuLeuGlyAlaAlaAr 303

Qy  500 AGAAGGGGCAGGAGGATGAACTGGAAGTCCGGGTCGGT 536
             :::||||                ::|||
Db  303 gArgArgLeuArgAlaAlaAspArgArgLeuArgProGly 315
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RESULT 14
US-09-252-991A-20615
; Sequence 20615, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;   APPLICANT: Marc J. Rubenfield et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;   TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 107196.136
;   CURRENT APPLICATION NUMBER: US/09/252,991A
;   CURRENT FILING DATE: 1999-02-18
;   PRIOR APPLICATION NUMBER: US 60/074,788
;   PRIOR FILING DATE: 1998-02-18
;   PRIOR APPLICATION NUMBER: US 60/094,190
;   PRIOR FILING DATE: 1998-07-27
;   NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20615
;   LENGTH: 164
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20615

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Alignment Scores:
Pred. No.:              0.0157
Score:                  105.00          Length:        164
Percent Similarity:     32.99%          Matches:       51
Best Local Similarity:  25.89%          Conservative:  14
                                        Mismatches:    68
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Query Match:       9.84%        Indels:    64         DB:                              4         Gaps:          10
DB:                4            Gaps:      10

US-10-659-782A-11 (1-579) x US-09-252-991A-20615 (1-164)          US-10-659-782A-11 (1-579) x US-09-252-991A-17910 (1-409)

Qy  574 CCCTCCTCGCTGCCACAGAGCATAAAACTGACAGAGTACCGACACCGGACTTCCAGTTCA 515     Qy  117 CTCCCCAGGACCGTCGCAGCCTCCGCTCCTCCGGCATGCTCCTCGCTGACTTGGCCCAT 176
        ||| ||| :::                :::||||||:::||||||||| |||                ||| :::                :::||| ::::|||
Db    7 ProGlySerThrProSerArg--------------ValProSerArgThrSerArgSer 21       Db  194 IleSerArgSerHisCysSerSerProProArgThrSerArgGlyMetGly--- 212

Qy  514 TCCTCTGCCCCT--------------- 503                                       Qy  177 GGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCCCACAA 236
        :::|||| |||                                                            |||
Db   22 AlaSerArgProCysSerIleAlaAlaThrTrpSerThrAlaAlaArgProMetPro 41         Db  213 ---------------------------ArgSerGlnGlyThrGlnArgGlySer 221

Qy  502 --TCTGCTGACCTGACCTGCTTCCGGGGCGGAGCCAGCCTGCTAGAGCTCGGGGGTGCAGC 446   Qy  237 AGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAAC------CAGTCTGTGACCTGGA 290
        ||||||||||   ||||||||||||||| |||||                             ||||||                           ||
Db   42 AsnSerAlaGlyProIleArgSerGlySerArgAlaMetArgArgArgAlaThrSer 61        Db  222 SerProAlaSerCysSerIleArgAlaArg--SerSerGlyCysArgAlaCysSerAlaSe 241

Qy  445 TTGGCTGGTGGCTTCTTCTTCGACTCCTTCTCTGCTGGAAGGGGGAAACAGTCTGTTTAGGA 386  Qy  291 GCAGCAGCGCCATCTC- 306
        |||                                                               ::: |||
Db   62 CysAla-------------------ThrTrpAlaGly- 67                          Db  241 rArgProArgArgSerMetAspAsnArgProThrArgThrArgGlurIleTh 261

Qy  385 CTCTAAGCCCCCATGTCCTTCCAGAAACAGTGAGTCAGACCCAGAGTCCTTTGTGCTCT 326  Qy  307 -------------TGGGCT---TCAGTCTCTCCCAGAGCACAAAGGACTCTCGGTC 347
        |||                                                  |||:::    :::|||||||
Db   68 -----------------------ThrProArgPro-------- 71                    Db  261 rPheSerAlaGluAsnTrpSerLeuSerGlnTyrGlnArgSerThrAlaAspSerGlyAr 281

Qy  325 GGGAGAAGACTGAAGCCCAGAGATGCGCGTGCTGCTCCAGGTCACAGAGCTGGTTGCTAA 266  Qy  348 TGACCTCACT-----------GTTCTGAAGGAACATGGGGGCTTAGAGTCCTAAACAG 395
        ||||||||| |||                                       :::|||||||
Db   72 GlyArgArgArgMetProArg-----ArgSerGlyProAlaThrArgCysArgCysSer 89   Db  281 gArgIleSerAlaIleIleArgLeuLeuGlyArgSerValProValArgSerAlaGlyAr 301

Qy  265 GTGGCAGGGCTGGAA------CAACATGTGGGGCTTGTGTGGGAGGTCTCCACCTGGACTC 212  Qy  396 ACTGTTTCCCCCT-----------TCCAGCAGAAAGGAGTCGAAGAAGCCACCAGCCAAG 446
        ||| ||||                     ::: |||                              |||||||:::|||
Db   90 ThrThrSerCysCysArgCysAlaArgThrSerSerAlaGlySerIleSerValArgPro 109  Db  301 gArgPheAlaProGluArgSerGlySerArgAspArgArg-CysValAlaAspA 321

Qy  211 TCTGGTGTTCAGGGCTCAGGAAGCTGGAGCCTGCCATGGCCCAGCTGGCCCAGCAGCATGC 152  Qy  447 CT------------GCAGCCCCGAGCTCTAGCAGGCTGGCTCCG---- 478
        :::||| :::||||||| |||                                 :: ||||||| :::|||
Db  110 ThrGly--ArgGlySerAlaSer------------------AlaProAlaArgSerThr 122  Db  321 laProThrAlaArgCysGlySerAlaProAlaArgSerArgProSerProArgArgGlyA 341

Qy  151 CGAGGAGCAGGAGGCTGCAGACGGTCCCTGGGAGGGCATGGCCTCAGCTGGGTTGCAGA 92  Qy  479 --------------------------------CCCGGA- 484
        |||                                                        ||||||
Db  123 AlaProMetTrpArgCysTrpProArgCysSerThrArgTrpProAlaArgSerAlaArg 142  Db  341 rgAspGlyGlySerArgArgArgAlaGlyArgLeuAlaGlyArgArgTrpTrpProGlyS 361

Qy   91 CAGGTGGGCCTCAGTCC---TGGCGGAGTGGTGCCTGTCGTGTCAGGTCT 44  Qy  485 ----------------------AGATGAGGTCAAGCAGCAGAAGGGCAGAGGGATGAACT- 520
        ::: |||||||| ::: :::   |||                                 |||||||||            |||
Db  143 ArgSerAlaAlaThrSerCysTrpPArgSerAlaSerAlaSerThrArgAla 159       Db  361 erGlyProAlaProArgArgLeuArgTrpArgTrpProArgArgProGlyArgGlyTrpSerA 381

                                                                         Qy  521 ------------GGAAGTCCGGGTCGG 535
                                                                                 ||||||||||||
                                                                         Db  381 laSerAspAlaArgHisArgArgAlaGlySerProGlyArg 394
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RESULT 15
US-09-252-991A-17910
; Sequence 17910, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT: Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT APPLICATION FILING DATE: 1999-02-18
;  PRIOR APPLICATION NUMBER: US 60/074,788
;  PRIOR APPLICATION FILING DATE: 1998-02-18
;  PRIOR APPLICATION NUMBER: US 60/094,190
;  PRIOR APPLICATION FILING DATE: 1998-07-27
;  NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17910
;  LENGTH: 409
;  TYPE: PRT
;  ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17910

Alignment Scores:
Pred. No.:            0.0225
Score:               105.00
Percent Similarity:   34.88%        Length:        409
Best Local Similarity: 25.12%       Matches:        54
Query Match:          10.19%        Conservative:   21
                                    Mismatches:     52
                                    Indels:         88
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Search completed: February 1, 2005, 13:30:31
Job time : 31.5 secs

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